

SCORE Search Results Details for Application 10764 and Search Result \$itemName.

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10764985 and Search Result \$itemName.
[start](#) | [next page](#)

[Go Back to pre](#)

			959		5	55.6	976	2	Q73SX6_MYCPA	Q73sx6 m
960	5	55.6	979	2	Q4DKR7_TRYCR				Q4dkr7 trypanosoma	
961	5	55.6	981	2	Q5AQL1_EMENI				Q5aql1 aspergillus	
962	5	55.6	982	2	Q54ZK5_DICDI				Q54zk5 dictyosteli	
963	5	55.6	982	2	Q2WC39_9VIRU				Q2wc39 enterobacte	
964	5	55.6	982	2	Q6UGD2_BPSP6				Q6ugd2 enterobacte	
965	5	55.6	989	2	Q4UGW0_THEAN				Q4ugw0 theileria a	
966	5	55.6	991	2	Q72SC6_LEPIC				Q72sc6 leptospira	
967	5	55.6	991	2	Q8F398_LEPIN				Q8f398 leptospira	
968	5	55.6	994	2	Q6CHE0_YARLI				Q6che0 yarrowia li	
969	5	55.6	1002	2	Q8EFG0_SHEON				Q8efg0 shewanella	
970	5	55.6	1003	2	Q9AHP2_9ACTO				Q9ahp2 arcanobacte	
971	5	55.6	1014	2	Q4Q946_LEIMA				Q4q946 leishmania	
972	5	55.6	1019	2	Q4Z9Z8_9CAUD				Q4z9z8 bacterioph	
973	5	55.6	1019	2	Q6Y7Q4_9CAUD				Q6y7q4 staphylococ	
974	5	55.6	1019	2	Q2PJW0_ENTFC				Q2pjw0 enterococcu	
975	5	55.6	1022	2	Q61907_CAEEL				Q61907 caenorhabdi	
976	5	55.6	1023	2	Q2T7E3_BURTH				Q2t7e3 burkholderi	
977	5	55.6	1028	2	Q5TML1_ANOGA				Q5tml1 anopheles g	
978	5	55.6	1034	2	Q6CX56_KLULA				Q6cx56 kluyveromyc	
979	5	55.6	1042	2	Q6D806_ERWC				Q6d806 erwinia car	
980	5	55.6	1044	2	Q9ZH24_PSEAE				Q9zh24 pseudomonas	
981	5	55.6	1045	2	Q9RG59_PSEAE				Q9rg59 pseudomonas	
982	5	55.6	1046	2	Q5A115_CANAL				Q5a115 candida alb	
983	5	55.6	1046	2	Q9ZNG8_PSEAE				Q9zng8 pseudomonas	
984	5	55.6	1053	2	Q6FQA8_CANGA				Q6fqa8 candida gla	
985	5	55.6	1070	2	Q7R2W4_GIALA				Q7r2w4 giardia lam	
986	5	55.6	1071	2	Q2Z867_9GAMM				Q2z867 shewanella	
987	5	55.6	1080	2	Q69PR5_ORYSA				Q69pr5 oryza sativ	
988	5	55.6	1083	2	Q43ZL3_SOLUS				Q43zl3 solibacter	
989	5	55.6	1084	2	Q2KEZ1_MAGGR				Q2kez1 magnaporthe	
990	5	55.6	1088	2	Q6ZUM6_HUMAN				Q6zum6 homo sapien	
991	5	55.6	1104	2	Q7MZ50_PHOLL				Q7mz50 photorhabdu	
992	5	55.6	1108	2	Q4ESI0_LISMO				Q4esi0 listeria mo	
993	5	55.6	1113	2	Q511P5_ENTHI				Q511p5 entamoeba h	
994	5	55.6	1117	2	Q388R2_9TRYP				Q388r2 trypanosoma	
995	5	55.6	1138	2	Q4H7T0_9DEIO				Q4h7t0 deinococcus	
996	5	55.6	1144	2	Q54BG8_DICDI				Q54bg8 dictyosteli	
997	5	55.6	1144	2	Q54ZA1_DICDI				Q54za1 dictyosteli	
998	5	55.6	1144	2	Q552I5_DICDI				Q552i5 dictyosteli	
999	5	55.6	1144	2	Q55D49_DICDI				Q55d49 dictyosteli	
1000	5	55.6	1144	2	Q9GQ49_DICDI				Q9gq49 dictyosteli	

ALIGNMENTS

RESULT 1
VHR2_CAMPM
ID VHR2_CAMPM STANDARD; PRT; 150 AA.
AC P68643; Q8V2Z8;
DT 07-DEC-2004, integrated into UniProtKB/Swiss-Prot.

DT 07-DEC-2004, sequence version 1.
 DT 07-FEB-2006, entry version 6.
 DE Probable host range protein 2.
 GN OrderedLocusNames=CMLV019;
 OS Camelpox virus (strain M-96).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=203173;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX MEDLINE=22031204; PubMed=12033760; DOI=10.1006/viro.2001.1343;
 RA Afonso C.L., Tulman E.R., Lu Z., Zsak L., Sandybaev N.T.,
 RA Kerembekova U.Z., Zaitsev V.L., Kutish G.F., Rock D.L.;
 RT "The genome of camelpox virus.";
 RL Virology 295:1-9 (2002).
 CC -!- FUNCTION: Plays a role for multiplication of the virus in
 CC different cell types (By similarity).
 CC -!- SIMILARITY: Belongs to the poxviruses C7 family.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AF438165; AAL73726.1; -; Genomic_DNA.
 DR InterPro; IPR004967; Pox_C7_F8A.
 DR Pfam; PF03287; Pox_C7_F8A; 1.
 DR PIRSF; PIRSF003779; VAC_C7L; 1.
 FT CHAIN 1 150 Probable host range protein 2.
 FT /FTId=PRO_0000099390.
 SQ SEQUENCE 150 AA; 18069 MW; 3D5557A68AF83D95 CRC64;

 Query Match 100.0%; Score 9; DB 1; Length 150;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 KVDDTFYVV 9
 |||||
 Db 74 KVDDTFYVV 82

RESULT 2
 VHR2_CAMPS
 ID VHR2_CAMPS STANDARD; PRT; 150 AA.
 AC P68642; Q8V2Z8;
 DT 07-DEC-2004, integrated into UniProtKB/Swiss-Prot.
 DT 07-DEC-2004, sequence version 1.
 DT 07-FEB-2006, entry version 6.
 DE Probable host range protein 2.
 GN OrderedLocusNames=CMP19L;
 OS Camelpox virus (strain CMS).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=203172;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX PubMed=11907336;
 RA Gubser C., Smith G.L.;
 RT "The sequence of camelpox virus shows it is most closely related to
 RT variola virus, the cause of smallpox.";
 RL J. Gen. Virol. 83:855-872(2002).
 CC -!- FUNCTION: Plays a role for multiplication of the virus in
 CC different cell types (By similarity).
 CC -!- SIMILARITY: Belongs to the poxviruses C7 family.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>

CC Distributed under the Creative Commons Attribution-NoDerivs License

CC -----

DR EMBL; AY009089; AAG37475.1; -; Genomic_DNA.

DR InterPro; IPR004967; Pox_C7_F8A.

DR Pfam; PF03287; Pox_C7_F8A; 1.

DR PIRSF; PIRSF003779; VAC_C7L; 1.

FT CHAIN 1 150 Probable host range protein 2.

FT /FTId=PRO_0000099391.

SQ SEQUENCE 150 AA; 18069 MW; 3D5557A68AF83D95 CRC64;

Query Match 100.0%; Score 9; DB 1; Length 150;

Best Local Similarity 100.0%; Pred. No. 0.014;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDTFYYV 9

|||||||

Db 74 KVDDTFYYV 82

RESULT 3

VHR2_VACCA

ID VHR2_VACCA STANDARD; PRT; 150 AA.

AC P68598; P17363; Q76ZY7;

DT 07-DEC-2004, integrated into UniProtKB/Swiss-Prot.

DT 07-DEC-2004, sequence version 1.

DT 07-FEB-2006, entry version 5.

DE Host range protein 2.

GN OrderedLocusNames=MVA018L, ACAM3000_MVA_018;

OS Vaccinia virus (strain Ankara) (VACV).

OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;

OC Orthopoxvirus.

OX NCBI_TaxID=126794;

RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RX MEDLINE=98263813; PubMed=9601507; DOI=10.1006/viro.1998.9123;

RA Antoine G., Scheiflinger F., Dorner F., Falkner F.G.;

RT "The complete genomic sequence of the modified vaccinia Ankara strain:

RT comparison with other orthopoxviruses.";

RL Virology 244:365-396(1998).

RN [2]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=Isolate Acambis 3000;

RA Esposito J.J., Frace M., Sammons S.A., Olsen-Rasmussen M.S.,

RA Osborne J., Khristova M., Wohlhueter R.M.;

RL Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.

CC -!- FUNCTION: Plays a role for multiplication of the virus in

CC different cell types (By similarity).

CC -!- SIMILARITY: Belongs to the poxviruses C7 family.

CC -----

CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>

CC Distributed under the Creative Commons Attribution-NoDerivs License

CC -----

DR EMBL; U94848; AAB96405.1; -; Genomic_DNA.

DR EMBL; AY603355; AAT10416.1; -; Genomic_DNA.

DR PIR; A33348; WZVZB1.

DR InterPro; IPR004967; Pox_C7_F8A.

DR Pfam; PF03287; Pox_C7_F8A; 1.

DR PIRSF; PIRSF003779; VAC_C7L; 1.

KW Early protein.

FT CHAIN 1 150 Host range protein 2.

FT /FTId=PRO_0000099386.

SQ SEQUENCE 150 AA; 17999 MW; 47CDF841D563C0A4 CRC64;

Query Match 100.0%; Score 9; DB 1; Length 150;

Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDTFYYV 9
 |||||||||
 Db 74 KVDDTFYYV 82

RESULT 4

VHR2_VACCC

ID VHR2_VACCC STANDARD; PRT; 150 AA.
 AC P68599; P17363;
 DT 07-DEC-2004, integrated into UniProtKB/Swiss-Prot.
 DT 07-DEC-2004, sequence version 1.
 DT 07-FEB-2006, entry version 5.
 DE Host range protein 2.
 GN ORFNames=C7L;
 OS Vaccinia virus (strain Copenhagen) (VACV).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=10249;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX MEDLINE=91021027; PubMed=2219722;
 RA Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
 RA Paoletti E.;
 RT "The complete DNA sequence of vaccinia virus.";
 RL Virology 179:247-266(1990).
 RN [2]
 RP COMPLETE GENOME.
 RA Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
 RA Paoletti E.;
 RT "Appendix to 'The complete DNA sequence of vaccinia virus'.";
 RL Virology 179:517-563(1990).
 CC -!- FUNCTION: Plays a role for multiplication of the virus in
 CC different cell types (By similarity).
 CC -!- SIMILARITY: Belongs to the poxviruses C7 family.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; M35027; AAA47993.1; -; Genomic_DNA.
 DR PIR; A33348; WZVZB1.
 DR InterPro; IPR004967; Pox_C7_F8A.
 DR Pfam; PF03287; Pox_C7_F8A; 1.
 DR PIRSF; PIRSF003779; VAC_C7L; 1.
 KW Early protein.
 FT CHAIN 1 150 Host range protein 2.
 FT /FTId=PRO_0000099387.
 SQ SEQUENCE 150 AA; 17999 MW; 47CDF841D563C0A4 CRC64;

Query Match 100.0%; Score 9; DB 1; Length 150;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDTFYYV 9
 |||||||||
 Db 74 KVDDTFYYV 82

RESULT 5

VHR2_VACCV

ID VHR2_VACCV STANDARD; PRT; 150 AA.
 AC P68600; P17363; Q76ZY7;

DT 07-DEC-2004, integrated into UniProtKB/Swiss-Prot.
 DT 07-DEC-2004, sequence version 1.
 DT 07-FEB-2006, entry version 7.
 DE Host range protein 2.
 GN OrderedLocusNames=VACWR021; ORFNames=C7L;
 OS Vaccinia virus (strain Western Reserve / WR) (VACV).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=10254;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RX MEDLINE=89073756; PubMed=2849238;
 RA Kotwal G.J., Moss B.;
 RT "Analysis of a large cluster of nonessential genes deleted from a
 RT vaccinia virus terminal transposition mutant.";
 RL Virology 167:524-537(1988).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RA Esposito J.J., Frace A.M., Sammons S.A., Olsen-Rasmussen M.,
 RA Osborne J., Wohlhueter R.;
 RT "Sequencing of the coding region of Vaccinia-WR to an average 9-fold
 RT redundancy and an error rate of 0.16/10kb.";
 RL Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP FUNCTION.
 RX MEDLINE=91021030; PubMed=2171207;
 RA Perkus M.E., Goebel S.J., Davis S.W., Johnson G.P., Limbach K.,
 RA Norton E.K., Paoletti E.;
 RT "Vaccinia virus host range genes.";
 RL Virology 179:276-286(1990).
 RN [4]
 RP FUNCTION.
 RX MEDLINE=93329391; PubMed=8336123;
 RA Oguriura N., Spehner D., Drillien R.;
 RT "Detection of a protein encoded by the vaccinia virus C7L open reading
 RT frame and study of its effect on virus multiplication in different
 RT cell lines.";
 RL J. Gen. Virol. 74:1409-1413(1993).
 CC -!- FUNCTION: Plays a role for multiplication of the virus in
 CC different cell types.
 CC -!- SIMILARITY: Belongs to the poxviruses C7 family.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; M22812; AAA69601.1; -; Genomic_DNA.
 DR EMBL; AY243312; AAO89300.1; -; Genomic_DNA.
 DR PIR; A33348; WZVZB1.
 DR InterPro; IPR004967; Pox_C7_F8A.
 DR Pfam; PF03287; Pox_C7_F8A; 1.
 DR PIRSF; PIRSF003779; VAC_C7L; 1.
 KW Early protein.
 FT CHAIN 1 150 Host range protein 2.
 FT /FTId=PRO_0000099388.
 SQ SEQUENCE 150 AA; 17999 MW; 47CDF841D563C0A4 CRC64;

Query Match 100.0%; Score 9; DB 1; Length 150;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDTFYVV 9
 |||||||||
 Db 74 KVDDTFYVV 82

SCORE Search Results Details for Application 10764 and Search Result \$itemName.

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10764985 and Search Result \$itemName.
[start](#) | [next page](#)

[Go Back to pre](#)

			959	5	55.6	976	2	Q73SX6_MYCPA	Q73sx6 m
960	5	55.6	979	2	Q4DKR7_TRYCR			Q4dkr7 trypanosoma	
961	5	55.6	981	2	Q5AQL1_EMENI			Q5aql1 aspergillus	
962	5	55.6	982	2	Q54ZK5_DICDI			Q54zk5 dictyosteli	
963	5	55.6	982	2	Q2WC39_9VIRU			Q2wc39 enterobacte	
964	5	55.6	982	2	Q6UGD2_BPSP6			Q6ugd2 enterobacte	
965	5	55.6	989	2	Q4UGW0_THEAN			Q4ugw0 theileria a	
966	5	55.6	991	2	Q72SC6_LEPIC			Q72sc6 leptospira	
967	5	55.6	991	2	Q8F398_LEPIN			Q8f398 leptospira	
968	5	55.6	994	2	Q6CHE0_YARLI			Q6che0 yarrowia li	
969	5	55.6	1002	2	Q8EFG0_SHEON			Q8efg0 shewanella	
970	5	55.6	1003	2	Q9AHP2_9ACTO			Q9ahp2 arcanobacte	
971	5	55.6	1014	2	Q4Q946_LEIMA			Q4q946 leishmania	
972	5	55.6	1019	2	Q4Z9Z8_9CAUD			Q4z9z8 bacteriopha	
973	5	55.6	1019	2	Q6Y7Q4_9CAUD			Q6y7q4 staphylococ	
974	5	55.6	1019	2	Q2PJW0_ENTFC			Q2pjw0 enterococcu	
975	5	55.6	1022	2	Q61907_CAEEL			Q61907 caenorhabdi	
976	5	55.6	1023	2	Q2T7E3_BURTH			Q2t7e3 burkholderi	
977	5	55.6	1028	2	Q5TML1_ANOGA			Q5tml1 anopheles g	
978	5	55.6	1034	2	Q6CX56_KLULA			Q6cx56 kluyveromyc	
979	5	55.6	1042	2	Q6D806_ERWCT			Q6d806 erwinia car	
980	5	55.6	1044	2	Q9ZH24_PSEAE			Q9zh24 pseudomonas	
981	5	55.6	1045	2	Q9RG59_PSEAE			Q9rg59 pseudomonas	
982	5	55.6	1046	2	Q5A115_CANAL			Q5a115 candida alb	
983	5	55.6	1046	2	Q9ZNG8_PSEAE			Q9zng8 pseudomonas	
984	5	55.6	1053	2	Q6FQA8_CANGA			Q6fqa8 candida gla	
985	5	55.6	1070	2	Q7R2W4_GIALA			Q7r2w4 giardia lam	
986	5	55.6	1071	2	Q2Z867_9GAMM			Q2z867 shewanella	
987	5	55.6	1080	2	Q69PR5_ORYSA			Q69pr5 oryza sativ	
988	5	55.6	1083	2	Q43ZL3_SOLUS			Q43zl3 solibacter	
989	5	55.6	1084	2	Q2KEZ1_MAGGR			Q2kez1 magnaporthe	
990	5	55.6	1088	2	Q6ZUM6_HUMAN			Q6zum6 homo sapien	
991	5	55.6	1104	2	Q7MZ50_PHOLL			Q7mz50 photorhabdu	
992	5	55.6	1108	2	Q4ESI0_LISMO			Q4esi0 listeria mo	
993	5	55.6	1113	2	Q511P5_ENTHI			Q511p5 entamoeba h	
994	5	55.6	1117	2	Q388R2_9TRYP			Q388r2 trypanosoma	
995	5	55.6	1138	2	Q4H7T0_9DEIO			Q4h7t0 deinococcus	
996	5	55.6	1144	2	Q54BG8_DICDI			Q54bg8 dictyosteli	
997	5	55.6	1144	2	Q54ZA1_DICDI			Q54za1 dictyosteli	
998	5	55.6	1144	2	Q552I5_DICDI			Q552i5 dictyosteli	
999	5	55.6	1144	2	Q55D49_DICDI			Q55d49 dictyosteli	
1000	5	55.6	1144	2	Q9GQ49_DICDI			Q9gq49 dictyosteli	

ALIGNMENTS

RESULT 1
VHR2_CAMPM
ID VHR2_CAMPM STANDARD; PRT; 150 AA.
AC P68643; Q8V2Z8;
DT 07-DEC-2004, integrated into UniProtKB/Swiss-Prot.

DT 07-DEC-2004, sequence version 1.
 DT 07-FEB-2006, entry version 6.
 DE Probable host range protein 2.
 GN OrderedLocusNames=CMLV019;
 OS Camelpox virus (strain M-96).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=203173;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX MEDLINE=22031204; PubMed=12033760; DOI=10.1006/viro.2001.1343;
 RA Afonso C.L., Tulman E.R., Lu Z., Zsak L., Sandybaev N.T.,
 RA Kerembekova U.Z., Zaitsev V.L., Kutish G.F., Rock D.L.;
 RT "The genome of camelpox virus.";
 RL Virology 295:1-9 (2002).
 CC -!- FUNCTION: Plays a role for multiplication of the virus in
 CC different cell types (By similarity).
 CC -!- SIMILARITY: Belongs to the poxviruses C7 family.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AF438165; AAL73726.1; -; Genomic_DNA.
 DR InterPro; IPR004967; Pox_C7_F8A.
 DR Pfam; PF03287; Pox_C7_F8A; 1.
 DR PIRSF; PIRSF003779; VAC_C7L; 1.
 FT CHAIN 1 150 Probable host range protein 2.
 FT /FTId=PRO_0000099390.
 SQ SEQUENCE 150 AA; 18069 MW; 3D5557A68AF83D95 CRC64;

Query Match 100.0%; Score 9; DB 1; Length 150;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KVDDTFYYY 9
 |||||
 Db 74 KVDDTFYYY 82

RESULT 2
 VHR2_CAMPS
 ID VHR2_CAMPS STANDARD; PRT; 150 AA.
 AC P68642; Q8V2Z8;
 DT 07-DEC-2004, integrated into UniProtKB/Swiss-Prot.
 DT 07-DEC-2004, sequence version 1.
 DT 07-FEB-2006, entry version 6.
 DE Probable host range protein 2.
 GN OrderedLocusNames=CMP19L;
 OS Camelpox virus (strain CMS).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=203172;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX PubMed=11907336;
 RA Gubser C., Smith G.L.;
 RT "The sequence of camelpox virus shows it is most closely related to
 RT variola virus, the cause of smallpox.";
 RL J. Gen. Virol. 83:855-872(2002).
 CC -!- FUNCTION: Plays a role for multiplication of the virus in
 CC different cell types (By similarity).
 CC -!- SIMILARITY: Belongs to the poxviruses C7 family.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>

CC Distributed under the Creative Commons Attribution-NoDerivs License

CC -----

DR EMBL; AY009089; AAG37475.1; -; Genomic_DNA.

DR InterPro; IPR004967; Pox_C7_F8A.

DR Pfam; PF03287; Pox_C7_F8A; 1.

DR PIRSF; PIRSF003779; VAC_C7L; 1.

FT CHAIN 1 150 Probable host range protein 2..

FT /FTId=PRO_0000099391.

SQ SEQUENCE 150 AA; 18069 MW; 3D5557A68AF83D95 CRC64;

Query Match 100.0%; Score 9; DB 1; Length 150;

Best Local Similarity 100.0%; Pred. No. 0.014;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDTFYYVV 9

|||||||

Db 74 KVDDTFYYVV 82

RESULT 3

VHR2_VACCA

ID VHR2_VACCA STANDARD; PRT; 150 AA.

AC P68598; P17363; Q76ZY7;

DT 07-DEC-2004, integrated into UniProtKB/Swiss-Prot.

DT 07-DEC-2004, sequence version 1.

DT 07-FEB-2006, entry version 5.

DE Host range protein 2.

GN OrderedLocusNames=MVA018L, ACAM3000_MVA_018;

OS Vaccinia virus (strain Ankara) (VACV).

OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;

OC Orthopoxvirus.

OX NCBI_TaxID=126794;

RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RX MEDLINE=98263813; PubMed=9601507; DOI=10.1006/viro.1998.9123;

RA Antoine G., Scheiflinger F., Dorner F., Falkner F.G.;

RT "The complete genomic sequence of the modified vaccinia Ankara strain:

RT comparison with other orthopoxviruses.";

RL Virology 244:365-396(1998).

RN [2]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=Isolate Acambis 3000;

RA Esposito J.J., Frace M., Sammons S.A., Olsen-Rasmussen M.S.,

RA Osborne J., Khristova M., Wohlhueter R.M.;

RL Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.

CC -!- FUNCTION: Plays a role for multiplication of the virus in
CC different cell types (By similarity).

CC -!- SIMILARITY: Belongs to the poxviruses C7 family.

CC -----

CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>

CC Distributed under the Creative Commons Attribution-NoDerivs License

CC -----

DR EMBL; U94848; AAB96405.1; -; Genomic_DNA.

DR EMBL; AY603355; AAT10416.1; -; Genomic_DNA.

DR PIR; A33348; WZVZB1.

DR InterPro; IPR004967; Pox_C7_F8A.

DR Pfam; PF03287; Pox_C7_F8A; 1.

DR PIRSF; PIRSF003779; VAC_C7L; 1.

KW Early protein.

FT CHAIN 1 150 Host range protein 2..

FT /FTId=PRO_0000099386.

SQ SEQUENCE 150 AA; 17999 MW; 47CDF841D563C0A4 CRC64;

Query Match 100.0%; Score 9; DB 1; Length 150;

Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDTFYYV 9
 |||||||||
 Db 74 KVDDTFYYV 82

RESULT 4

VHR2_VACCC

ID VHR2_VACCC STANDARD; PRT; 150 AA.
 AC P68599; P17363;
 DT 07-DEC-2004, integrated into UniProtKB/Swiss-Prot.
 DT 07-DEC-2004, sequence version 1.
 DT 07-FEB-2006, entry version 5.
 DE Host range protein 2.
 GN ORFNames=C7L;
 OS Vaccinia virus (strain Copenhagen) (VACV).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=10249;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX MEDLINE=91021027; PubMed=2219722;
 RA Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
 RA Paoletti E.;
 RT "The complete DNA sequence of vaccinia virus.";
 RL Virology 179:247-266(1990).
 RN [2]
 RP COMPLETE GENOME.
 RA Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
 RA Paoletti E.;
 RT "Appendix to 'The complete DNA sequence of vaccinia virus'.";
 RL Virology 179:517-563(1990).
 CC -!- FUNCTION: Plays a role for multiplication of the virus in
 CC different cell types (By similarity).
 CC -!- SIMILARITY: Belongs to the poxviruses C7 family.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; M35027; AAA47993.1; -; Genomic_DNA.
 DR PIR; A33348; WZVZB1.
 DR InterPro; IPR004967; Pox_C7_F8A.
 DR Pfam; PF03287; Pox_C7_F8A; 1.
 DR PIRSF; PIRSF003779; VAC_C7L; 1.
 KW Early protein.
 FT CHAIN 1 150 Host range protein 2.
 FT /FTId=PRO_0000099387.
 SQ SEQUENCE 150 AA; 17999 MW; 47CDF841D563C0A4 CRC64;

Query Match 100.0%; Score 9; DB 1; Length 150;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDTFYYV 9
 |||||||||
 Db 74 KVDDTFYYV 82

RESULT 5

VHR2_VACCV

ID VHR2_VACCV STANDARD; PRT; 150 AA.
 AC P68600; P17363; Q76ZY7;

DT 07-DEC-2004, integrated into UniProtKB/Swiss-Prot.
 DT 07-DEC-2004, sequence version 1.
 DT 07-FEB-2006, entry version 7.
 DE Host range protein 2.
 GN OrderedLocusNames=VACWR021; ORFNames=C7L;
 OS Vaccinia virus (strain Western Reserve / WR) (VACV).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=10254;
 [1]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RX MEDLINE=89073756; PubMed=2849238;
 RA Kotwal G.J., Moss B.;
 RT "Analysis of a large cluster of nonessential genes deleted from a
 RT vaccinia virus terminal transposition mutant.";
 RL Virology 167:524-537(1988).
 [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RA Esposito J.J., Frace A.M., Sammons S.A., Olsen-Rasmussen M.,
 RA Osborne J., Wohlhueter R.;
 RT "Sequencing of the coding region of Vaccinia-WR to an average 9-fold
 RT redundancy and an error rate of 0.16/10kb.";
 RL Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
 [3]
 RP FUNCTION.
 RX MEDLINE=91021030; PubMed=2171207;
 RA Perkus M.E., Goebel S.J., Davis S.W., Johnson G.P., Limbach K.,
 RA Norton E.K., Paoletti E.;
 RT "Vaccinia virus host range genes.";
 RL Virology 179:276-286(1990).
 [4]
 RP FUNCTION.
 RX MEDLINE=93329391; PubMed=8336123;
 RA Oguiura N., Spehner D., Drillien R.;
 RT "Detection of a protein encoded by the vaccinia virus C7L open reading
 RT frame and study of its effect on virus multiplication in different
 RT cell lines.";
 RL J. Gen. Virol. 74:1409-1413(1993).
 CC -!- FUNCTION: Plays a role for multiplication of the virus in
 CC different cell types.
 CC -!- SIMILARITY: Belongs to the poxviruses C7 family.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; M22812; AAA69601.1; -; Genomic_DNA.
 DR EMBL; AY243312; AAO89300.1; -; Genomic_DNA.
 DR PIR; A33348; WZVZB1.
 DR InterPro; IPR004967; Pox_C7_F8A.
 DR Pfam; PF03287; Pox_C7_F8A; 1.
 DR PIRSF; PIRSF003779; VAC_C7L; 1.
 KW Early protein.
 FT CHAIN 1 150 Host range protein 2.
 FT /FTId=PRO_0000099388.
 SQ SEQUENCE 150 AA; 17999 MW; 47CDF841D563C0A4 CRC64;

Query Match 100.0%; Score 9; DB 1; Length 150;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDTFYVV 9
 |||||
 Db 74 KVDDTFYVV 82

RESULT 6

VHR2_VARV

ID VHR2_VARV STANDARD; PRT; 150 AA.
 AC P33860;
 DT 01-FEB-1994, integrated into UniProtKB/Swiss-Prot.
 DT 01-FEB-1994, sequence version 1.
 DT 07-FEB-2006, entry version 30.
 DE Host range protein 2.
 GN ORFNames=C7L, B15L, D8L;
 OS Variola virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=10255;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RC STRAIN=India-1967 / Isolate Ind3;
 RX MEDLINE=93202281; PubMed=8384129; DOI=10.1016/0014-5793(93)80041-R;
 RA Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.;
 RT "Genes of variola and vaccinia viruses necessary to overcome the host
 protective mechanisms.";
 RL FEBS Lett. 319:80-83(1993).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RC STRAIN=Bangladesh-1975;
 RX MEDLINE=94088747; PubMed=8264798; DOI=10.1038/366748a0;
 RA Massung R.F., Esposito J.J., Liu L.I., Qi J., Utterback T.R.,
 RA Knight J.C., Aubin L., Yuran T.E., Parsons J.M., Loparev V.N.,
 RA Selivanov N.A., Cavallaro K.F., Kerlavage A.R., Mahy B.W.J.,
 RA Venter C.J.;
 RT "Potential virulence determinants in terminal regions of variola
 smallpox virus genome.";
 RL Nature 366:748-751(1993).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RC STRAIN=Congo-1965, Garcia-1966, and Somalia-1977;
 RA Massung R.F., Loparev V.N., Knight J.C., Chizhikov V.E., Parsons J.M.,
 RA Totmenin A.V., Shchelkunov S.N., Esposito J.J.;
 RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Plays a role for multiplication of the virus in
 CC different cell types (By similarity).
 CC -!- SIMILARITY: Belongs to the poxviruses C7 family.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; X69198; CAA48949.1; -; Genomic_DNA.
 DR EMBL; L22579; AAA60756.1; -; Genomic_DNA.
 DR EMBL; U18340; AAA69419.1; -; Genomic_DNA.
 DR EMBL; U18337; AAA69313.1; -; Genomic_DNA.
 DR EMBL; U18338; AAA69354.1; -; Genomic_DNA.
 DR PIR; F72151; F72151.
 DR PIR; H36837; H36837.
 DR PIR; T28446; T28446.
 DR InterPro; IPR004967; Pox_C7_F8A.
 DR Pfam; PF03287; Pox_C7_F8A; 1.
 DR PIRSF; PIRSF003779; VAC_C7L; 1.
 FT CHAIN 1 150 Host range protein 2.
 FT /FTId=PRO_0000099389.
 SQ SEQUENCE 150 AA; 18027 MW; 50FDF841C253CE94 CRC64;

Query Match 100.0%; Score 9; DB 1; Length 150;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDTFYYV 9
 |||||||||
 Db 74 KVDDTFYYV 82

RESULT 7

Q49QR1_9POXV
 ID Q49QR1_9POXV PRELIMINARY; PRT; 150 AA.
 AC Q49QR1;
 DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
 DT 13-SEP-2005, sequence version 1.
 DT 07-FEB-2006, entry version 6.
 DE Hypothetical protein.
 GN ORFNames=m8020L, m0020L;
 OS Vaccinia virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=10245;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=LC16m8, and LC16m0;
 RX PubMed=16140764; DOI=10.1128/JVI.79.18.11873-11891.2005;
 RA Morikawa S., Sakiyama T., Hasegawa H., Saijo M., Maeda A., Kurane I.,
 RA Maeno G., Kimura J., Hirama C., Yoshida T., Asahi-Ozaki Y., Sata T.,
 RA Kurata T., Kojima A.;
 RT "An attenuated LC16m8 smallpox vaccine: analysis of full-genome
 sequence and induction of immune protection.";
 RL J. Virol. 79:11873-11891(2005).
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AY678275; AAW23413.1; -; Genomic_DNA.
 DR EMBL; AY678277; AAW23695.1; -; Genomic_DNA.
 DR GO; GO:0016032; P:viral life cycle; IEA.
 DR InterPro; IPR004967; Pox_C7_F8A.
 DR Pfam; PF03287; Pox_C7_F8A; 1.
 DR PIRSF; PIRSF003779; VAC_C7L; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 150 AA; 17999 MW; 47CDF841D563C0A4 CRC64;

Query Match 100.0%; Score 9; DB 2; Length 150;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDTFYYV 9
 |||||||||
 Db 74 KVDDTFYYV 82

RESULT 8

Q6RZS8_9POXV
 ID Q6RZS8_9POXV PRELIMINARY; PRT; 150 AA.
 AC Q6RZS8;
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 9.
 DE RPXV013.
 GN ORFNames=RPXV013;
 OS Rabbitpox virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=32606;

RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=16227218; DOI=10.1099/vir.0.81331-0;
 RA Li G., Chen N., Roper R.L., Feng Z., Hunter A., Danila M.,
 RA Lefkowitz E.J., Buller R.M., Upton C.;
 RT "Complete coding sequences of the rabbitpox virus genome.";
 RL J. Gen. Virol. 86:2969-2977(2005).
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AY484669; AAS49726.1; -; Genomic_DNA.
 DR GO; GO:0016032; P:viral life cycle; IEA.
 DR InterPro; IPR004967; Pox_C7_F8A.
 DR Pfam; PF03287; Pox_C7_F8A; 1.
 DR PIRSF; PIRSF003779; VAC_C7L; 1.
 SQ SEQUENCE 150 AA; 17999 MW; 47CDF841D563C0A4 CRC64;

Query Match 100.0%; Score 9; DB 2; Length 150;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDTFYYV 9
 |||||
 Db 74 KVDDTFYYV 82

RESULT 9
 Q76Q66_VARV
 ID Q76Q66_VARV PRELIMINARY; PRT; 150 AA.
 AC Q76Q66;
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 8.
 DE B14L protein.
 GN Name=B14L;
 OS Variola minor virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=53258;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Garcia-1966;
 RA Shchelkunov S.N., Totmenin A.V., Gutorov V.V., Safronov P.F.,
 RA Massung R.F., Loparev V.N., Knight J.C., Chizhikov V.E., Parsons J.M.,
 RA Esposito J.J., Sosnovtsev S.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; Y16780; CAB54608.1; -; Genomic_DNA.
 DR GO; GO:0016032; P:viral life cycle; IEA.
 DR InterPro; IPR004967; Pox_C7_F8A.
 DR Pfam; PF03287; Pox_C7_F8A; 1.
 DR PIRSF; PIRSF003779; VAC_C7L; 1.
 SQ SEQUENCE 150 AA; 18027 MW; 5QFDF841C253CE94 CRC64;

Query Match 100.0%; Score 9; DB 2; Length 150;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDTFYYV 9

Db 74 KVDDTFYYV 82

RESULT 10

Q76QL6_COWPX

ID Q76QL6_COWPX PRELIMINARY; PRT; 150 AA.

AC Q76QL6;

DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.

DT 05-JUL-2004, sequence version 1.

DT 07-FEB-2006, entry version 9.

DE C13L protein.

GN Name=C13L;

OS Cowpox virus (CPV).

OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;

OC Orthopoxvirus.

OX NCBI_TaxID=10243;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=GRI-90;

RX MEDLINE=97068532; PubMed=8963248;

RA Safronov P.F., Petrov N.A., Riazankina O.I., Totmenin A.V.,

RA Shchelkunov S.N., Sandakhchiev L.S.;

RT "Genes of a circle of hosts for the cowpox virus.";

RL Dokl. Akad. Nauk SSSR 349:829-833(1996).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=GRI-90;

RX MEDLINE=98229462; PubMed=9568042; DOI=10.1006/viro.1998.9039;

RA Shchelkunov S.N., Safronov P.F., Totmenin A.V., Petrov N.A.,

RA Riazankina O.I., Gutorov V.V., Kotwal G.J.,

RT "The genomic sequence analysis of the left and right species-specific

RT terminal region of a cowpox virus strain reveals unique sequences and

RT a cluster of intact ORFs for immunomodulatory and host range

RT proteins.";

RL Virology 243:432-460(1998).

RN [3]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=GRI-90;

RA Shchelkunov S.N., Safronov P.F., Totmenin A.V., Miheev M.V.,

RA Riazankina O.I., Petrov N.A., Gutorov V.V., Kotwal G.J.,

RA Sandakhchiev L.S.;

RL Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

CC -----

CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>

CC Distributed under the Creative Commons Attribution-NoDerivs License

CC -----

DR EMBL; X94355; CAA64098.1; -; Genomic_DNA.

DR GO; GO:0016032; P:viral life cycle; IEA.

DR InterPro; IPR004967; Pox_C7_F8A.

DR Pfam; PF03287; Pox_C7_F8A; 1.

DR PIRSF; PIRSF003779; VAC_C7L; 1.

SQ SEQUENCE 150 AA; 17999 MW; 47CDF841D563C0A4 CRC64;

Query Match 100.0%; Score 9; DB 2; Length 150;

Best Local Similarity 100.0%; Pred. No. 0.014;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVDDTFYYV 9

|||||||

Db 74 KVDDTFYYV 82

RESULT 11

Q77TN9_VACCT

ID Q77TN9_VACCT PRELIMINARY; PRT; 150 AA.
 AC Q77TN9;
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 8.
 DE TC7L.
 OS Vaccinia virus (strain Tian Tan) (VACV).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=10253;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Tian Tan;
 RA Jin Q., Hou Y.D., Cheng N.H., Yao E.M., Cheng S.X., Yang X.K.,
 RA Jing D.Y., Yu W.H., Yuan J.S., Ma X.J.;
 RL Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AF095689; AAF33872.1; -, Genomic_DNA.
 DR GO; GO:0016032; P:viral life cycle; IEA.
 DR InterPro; IPR004967; Pox_C7_F8A.
 DR Pfam; PF03287; Pox_C7_F8A; 1.
 DR PIRSF; PIRSF003779; VAC_C7L; 1.
 SQ SEQUENCE 150 AA; 17999 MW; 47CDF841D563C0A4 CRC64;

Query Match 100.0%; Score 9; DB 2; Length 150;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KVDDTFYYV 9
 |||||
 Db 74 KVDDTFYYV 82

RESULT 12
 Q8JLI7_9POXV
 ID Q8JLI7_9POXV PRELIMINARY; PRT; 150 AA.
 AC Q8JLI7;
 DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
 DT 01-OCT-2002, sequence version 1.
 DT 07-FEB-2006, entry version 12.
 DE EVM015.
 GN Name=EVM015;
 OS Ectromelia virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=12643;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Moscow;
 RX MEDLINE=95266283; PubMed=7747448;
 RA Mossman K., Upton C., Buller R.M., McFadden G.;
 RT "Species specificity of ectromelia virus and vaccinia virus
 RT interferon-gamma binding proteins.";
 RL Virology 208:762-769 (1995).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Moscow;
 RX MEDLINE=20192152; PubMed=10725549; DOI=10.1016/S0168-1702(99)00135-5;
 RA Chen N., Buller R.M., Wall E.M., Upton C.;
 RT "Analysis of host response modifier ORFs of ectromelia virus, the
 RT causative agent of mousepox.";

RL Virus Res. 66:155-173(2000).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Moscow;
 RX MEDLINE=98154919; PubMed=9495531; DOI=10.1016/S0168-1702(97)00122-6;
 RA Wall E.M., Cao J.X., Chen N., Buller R.M.L., Upton C.;
 RT "A novel poxvirus gene and its human homolog are similar to an *E. coli*
 RT lysophospholipase.";
 RL Virus Res. 52:157-167(1997).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Moscow;
 RA Chen N., Danila M.I., Feng Z., Buller M.L., Wang C., Han X.,
 RA Lefkowitz E., Upton C.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AF012825; AAM92321.1; -; Genomic_DNA.
 DR GO; GO:0016032; P:viral life cycle; IEA.
 DR InterPro; IPR004967; Pox_C7_F8A.
 DR Pfam; PF03287; Pox_C7_F8A; 1.
 DR PIRSF; PIRSF003779; VAC_C7L; 1.
 SQ SEQUENCE 150 AA; 18130 MW; 4DD4FC55F62422BE CRC64;

Query Match 100.0%; Score 9; DB 2; Length 150;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDTFYYY 9
 |||||
 Db 74 KVDDTFYYY 82

RESULT 13

Q8QN33_COWPX
 ID Q8QN33_COWPX PRELIMINARY; PRT; 150 AA.
 AC Q8QN33;
 DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
 DT 01-JUN-2002, sequence version 1.
 DT 07-FEB-2006, entry version 10.
 DE CPXV029 protein.
 GN Name=CPXV029 CDS;
 OS Cowpox virus (CPV).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=10243;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Brighton Red;
 RX MEDLINE=83117629; PubMed=6961398;
 RA Pickup D.J., Bastia D., Stone H.O., Joklik W.K.;
 RT "Sequence of terminal regions of cowpox virus DNA: arrangement of
 RT repeated and unique sequence elements.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:7112-7116(1982).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Brighton Red;
 RX MEDLINE=90177240; PubMed=2309453;
 RA Parsons B.L., Pickup D.J.;
 RT "Transcription of orthopoxvirus telomeres at late times during
 RT infection.";
 RL Virology 175:69-80(1990).

RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Brighton Red;
 RX MEDLINE=91196263; PubMed=2014645;
 RA Hu F.Q., Pickup D.J.;
 RT "Transcription of the terminal loop region of vaccinia virus DNA is
 RT initiated from the telomere sequences directing DNA resolution.";
 RL Virology 181:716-720(1991).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Brighton Red;
 RX MEDLINE=94378510; PubMed=8091665;
 RA Hu F.Q., Smith C.A., Pickup D.J.;
 RT "Cowpox virus contains two copies of an early gene encoding a soluble
 RT secreted form of the type II TNF receptor.";
 RL Virology 204:343-356(1994).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Brighton Red;
 RA Dietrich F.S., Ray C.A., Sharma D.A., Allen A., Pickup D.J.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AF482758; AAM13476.1; -; Genomic_DNA.
 DR GO; GO:0016032; P:viral life cycle; IEA.
 DR InterPro; IPR004967; Pox_C7_F8A.
 DR Pfam; PF03287; Pox_C7_F8A; 1.
 DR PIRSF; PIRSF003779; VAC_C7L; 1.
 SQ SEQUENCE 150 AA; 17954 MW; 6B5C029714B02944 CRC64;

Query Match 100.0%; Score 9; DB 2; Length 150;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDTFYYY 9
 ||||| |||||
 Db 74 KVDDTFYYY 82

RESULT 14
 Q4WIR3_ASPFU
 ID Q4WIR3_ASPFU PRELIMINARY; PRT; 512 AA.
 AC Q4WIR3;
 DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2005, sequence version 1.
 DT 07-MAR-2006, entry version 6.
 DE Possible beta-xylosidase, family 43 of glycosyl hydrolases.
 GN ORFNames=Afu2g00930;
 OS Aspergillus fumigatus (Sartorya fumigata).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=5085;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Af293 / CBS 101355 / FGSC A1100;
 RX PubMed=16372009; DOI=10.1038/nature04332;
 RA Nierman W.C., Pain A., Anderson M.J., Wortman J.R., Kim H.S.,
 RA Arroyo J., Beriman M., Abe K., Archer D.B., Bermejo C., Bennett J.W.,
 RA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,
 RA Farman M., Fedorova N., Fedorova N.D., Feldblyum T.V., Fischer R.,
 RA Fosker N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
 RA Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.J.,

RA Haas H., Harris D.E., Horiuchi H., Huang J., Humphray S., Jimenez J.,
 RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Konzack S.,
 RA Kulkarni R., Kumagai T., Lafhton A., Latge J.-P., Li W., Lord A.,
 RA Lu C., Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M.,
 RA Monod M., Mouyna I., Mulligan S., Murphy L.D., O'Neil S., Paulsen I.,
 RA Penalva M.A., Pertea M., Price C., Pritchard B.L., Quail M.A.,
 RA Rabbinowitsch E., Rawlins N., Rajandream M.A., Reichard U.,
 RA Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
 RA Ronning C.M., Rutter S., Salzberg S.L., Sanchez M.,
 RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
 RA Takeuchi M., Tekiaia F., Turner G., Vazquez de Aldana C.R., Weidman J.,
 RA White O., Woodward J.R., Yu J.-H., Fraser C.M., Galagan J.E., Asai K.,
 RA Machida M., Hall N., Barrell B.G., Denning D.W.;
 RT "Genomic sequence of the pathogenic and allergenic filamentous fungus
 RT *Aspergillus fumigatus*.";
 RL Nature 438:1151-1156 (2005).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License.
 CC -----
 DR EMBL; AAHF01000008; EAL87192.1; -; Genomic_DNA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . . ; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 KW Complete proteome; Hydrolase.
 SQ SEQUENCE 512 AA; 55648 MW; 5E174A037C55B830 CRC64;

Query Match 77.8%; Score 7; DB 2; Length 512;
 Best Local Similarity 100.0%; Pred. No. 7.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTFYY 8
 |||||
 Db 26 VDDTFYY 32

RESULT 15
 Q2U7D1_ASPO
 ID Q2U7D1_ASPO PRELIMINARY; PRT; 515 AA.
 AC Q2U7D1;
 DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
 DT 24-JAN-2006, sequence version 1.
 DT 07-MAR-2006, entry version 3.
 DE Beta-xylosidase.
 GN ORFNames=AO090701000886;
 OS Aspergillus oryzae.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=5062;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=RIB 40;
 RX PubMed=16372010; DOI=10.1038/nature04300;
 RA Machida M., Asai K., Sano M., Tanaka T., Kumagai T., Terai G.,
 RA Kusumoto K., Arima T., Akita O., Kashiwagi Y., Abe K., Gomi K.,
 RA Horiuchi H., Kitamoto K., Kobayashi T., Takeuchi M., Denning D.W.,
 RA Galagan J.E., Nierman W.C., Yu J., Archer D.B., Bennett J.W.,
 RA Bhatnagar D., Cleveland T.E., Fedorova N.D., Gotoh O., Horikawa H.,
 RA Hosoyama A., Ichinomiya M., Igarashi R., Iwashita K., Juvvadi P.R.,
 RA Kato M., Kato Y., Kin T., Kokubun A., Maeda H., Maeyama N.,
 RA Maruyama J., Nagasaki H., Nakajima T., Oda K., Okada K., Paulsen I.,

RA Sakamoto K., Sawano T., Takahashi M., Takase K., Terabayashi Y.,
 RA Wortman J.R., Yamada O., Yamagata Y., Anazawa H., Hata Y., Koide Y.,
 RA Komori T., Koyama Y., Minetoki T., Suharnan S., Tanaka A., Isono K.,
 RA Kuwara S., Ogasawara N., Kikuchi H.;
 RT "Genome sequencing and analysis of *Aspergillus oryzae*.";
 RL *Nature* 438:1157-1161(2005).

CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----

DR EMBL; AP007164; BAE62534.1; -; Genomic_DNA.

SQ SEQUENCE 515 AA; 56635 MW; 3EDFD2B09FF52176 CRC64;

Query Match 77.8%; Score 7; DB 2; Length 515;
 Best Local Similarity 100.0%; Pred. No. 7.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTFYY 8
 |||||
 Db 39 VDDTFYY 45

RESULT 16

P73845_SYNY3

ID P73845_SYNY3 PRELIMINARY; PRT; 770 AA.

AC P73845;

DT 01-FEB-1997, integrated into UniProtKB/TrEMBL.

DT 01-FEB-1997, sequence version 1.

DT 07-FEB-2006, entry version 26.

DE Sll1608 protein.

GN OrderedLocusNames=sll1608;

OS Synechocystis sp. (strain PCC 6803).

OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.

OX NCBI_TaxID=1148;

RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RX MEDLINE=97061201; PubMed=8905231; DOI=10.1093/dnare/3.3.109;

RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,

RA Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,

RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,

RA Shimpoo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,

RA Tabata S.;

RT "Sequence analysis of the genome of the unicellular cyanobacterium

RT *Synechocystis* sp. strain PCC6803. II. Sequence determination of the

RT entire genome and assignment of potential protein-coding regions.";

RL DNA Res. 3:109-136(1996).

CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----

DR EMBL; BA000022; BAA17904.1; -; Genomic_DNA.

DR PIR; S75042; S75042.

DR BioCyc; SSP1148:SLL1608-MONOMER; -.

DR InterPro; IPR002931; Trnsglumase_like.

DR Pfam; PF01841; Transglut_core; 1.

DR SMART; SM00460; TGc; 1.

KW Complete proteome.

SQ SEQUENCE 770 AA; 87815 MW; F58C2EA34EC8873C CRC64;

Query Match 77.8%; Score 7; DB 2; Length 770;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTFYY 8

Db |||||
 286 VDDTFYY 292

RESULT 17
 Q8VUW8_STAHO
 ID Q8VUW8_STAHO PRELIMINARY; PRT; 103 AA.
 AC Q8VUW8;
 DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
 DT 01-MAR-2002, sequence version 1.
 DT 07-FEB-2006, entry version 9.
 DE ORF19.
 OS Staphylococcus hominis.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1290;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=GIFU12263;
 RX MEDLINE=22586405; PubMed=12700250;
 RX DOI=10.1128/JB.185.9.2711-2722.2003;
 RA Katayama Y., Takeuchi F., Ito T., Ma X.X., Ui-Mizutani Y.,
 RA Kobayashi I., Hiramatsu K.;
 RT "Identification in methicillin-susceptible Staphylococcus hominis of
 an active primordial mobile genetic element for the staphylococcal
 RT cassette chromosome mec of methicillin-resistant Staphylococcus
 RT aureus.";
 RL J. Bacteriol. 185:2711-2722(2003).
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AB063171; BAB83490.1; -; Genomic_DNA.
 DR InterPro; IPR009303; DUF960_STA_spp.
 DR Pfam; PF06124; DUF960; 1.
 SQ SEQUENCE 103 AA; 12599 MW; 13194326CCE4617D CRC64;

Query Match 66.7%; Score 6; DB 2; Length 103;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DTFYYV 9
 |||||
 Db 91 DTFYYV 96

RESULT 18
 Q38248_9CAUD
 ID Q38248_9CAUD PRELIMINARY; PRT; 126 AA.
 AC Q38248;
 DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
 DT 01-NOV-1996, sequence version 1.
 DT 07-FEB-2006, entry version 16.
 DE DNA polymerase subunit.
 OS Lactococcus phage bIL67.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
 OC c2-like viruses.
 OX NCBI_TaxID=36343;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=95111629; PubMed=7812447;
 RA Schouler C., Ehrlich S.D., Chopin M.C.;
 RT "Sequence and organization of the lactococcal prolate-headed bIL67
 RT phage genome.";
 RL Microbiology 140:3061-3069(1994).

CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; L33769; AAA74342.1; -; Genomic_DNA.
 SQ SEQUENCE 126 AA; 14843 MW; 1768C9622ED7749B CRC64;

Query Match 66.7%; Score 6; DB 2; Length 126;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDTF 6
 | | | | |
 Db 100 KVDDTF 105

RESULT 19

Q5A2T5_CANAL

ID Q5A2T5_CANAL PRELIMINARY; PRT; 176 AA.
 AC Q5A2T5;
 DT 26-APR-2005, integrated into UniProtKB/TrEMBL.
 DT 26-APR-2005, sequence version 1.
 DT 07-FEB-2006, entry version 7.
 DE Hypothetical protein.
 GN ORFNames=CaO19.2181, CaO19.9727;
 OS Candida albicans SC5314.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 OX NCBI_TaxID=237561;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=SC5314;
 RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
 RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
 RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
 RA Davis R.W., Scherer S.;
 RT "The diploid genome sequence of Candida albicans.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AACQ01000075; EAK97013.1; -; Genomic_DNA.
 DR EMBL; AACQ01000076; EAK96954.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 176 AA; 19448 MW; D04B9BE79CA86853 CRC64;

Query Match 66.7%; Score 6; DB 2; Length 176;
 Best Local Similarity 100.0%; Pred. No. 45;

[start](#) | [next page](#)

RESULT 6

VHR2_VARV

ID VHR2_VARV STANDARD; PRT; 150 AA.
 AC P33860;
 DT 01-FEB-1994, integrated into UniProtKB/Swiss-Prot.
 DT 01-FEB-1994, sequence version 1.
 DT 07-FEB-2006, entry version 30.
 DE Host range protein 2.
 GN ORFNames=C7L, B15L, D8L;
 OS Variola virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=10255;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RC STRAIN=India-1967 / Isolate Ind3;
 RX MEDLINE=93202281; PubMed=8384129; DOI=10.1016/0014-5793(93)80041-R;
 RA Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.;
 RT "Genes of variola and vaccinia viruses necessary to overcome the host
 protective mechanisms.";
 RL FEBS Lett. 319:80-83 (1993).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RC STRAIN=Bangladesh-1975;
 RX MEDLINE=94088747; PubMed=8264798; DOI=10.1038/366748a0;
 RA Massung R.F., Esposito J.J., Liu L.I., Qi J., Utterback T.R.,
 RA Knight J.C., Aubin L., Yuran T.E., Parsons J.M., Loparev V.N.,
 RA Selivanov N.A., Cavallaro K.F., Kerlavage A.R., Mahy B.W.J.,
 RA Venter C.J.;
 RT "Potential virulence determinants in terminal regions of variola
 smallpox virus genome.";
 RL Nature 366:748-751 (1993).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RC STRAIN=Congo-1965, Garcia-1966, and Somalia-1977;
 RA Massung R.F., Loparev V.N., Knight J.C., Chizhikov V.E., Parsons J.M.,
 RA Totmenin A.V., Shchelkunov S.N., Esposito J.J.;
 RL Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: Plays a role for multiplication of the virus in
 CC different cell types (By similarity).
 CC -!- SIMILARITY: Belongs to the poxviruses C7 family.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; X69198; CAA48949.1; -; Genomic_DNA.
 DR EMBL; L22579; AAA60756.1; -; Genomic_DNA.
 DR EMBL; U18340; AAA69419.1; -; Genomic_DNA.
 DR EMBL; U18337; AAA69313.1; -; Genomic_DNA.
 DR EMBL; U18338; AAA69354.1; -; Genomic_DNA.
 DR PIR; F72151; F72151.
 DR PIR; H36837; H36837.
 DR PIR; T28446; T28446.
 DR InterPro; IPR004967; Pox_C7_F8A.
 DR Pfam; PF03287; Pox_C7_F8A; 1.
 DR PIRSF; PIRSF003779; VAC_C7L; 1.
 FT CHAIN 1 150 Host range protein 2.
 FT /FTId=PRO_0000099389.
 SQ SEQUENCE 150 AA; 18027 MW; 50FDF841C253CE94 CRC64;

Query Match 100.0%; Score 9; DB 1; Length 150;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDTFYYY 9
 |||||||||
 Db 74 KVDDTFYYY 82

RESULT 7

Q49QR1_9POXV
 ID Q49QR1_9POXV PRELIMINARY; PRT; 150 AA.
 AC Q49QR1;
 DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
 DT 13-SEP-2005, sequence version 1.
 DT 07-FEB-2006, entry version 6.
 DE Hypothetical protein.
 GN ORFNames=m8020L, m0020L;
 OS Vaccinia virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=10245;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=LC16m8, and LC16m0;
 RX PubMed=16140764; DOI=10.1128/JVI.79.18.11873-11891.2005;
 RA Morikawa S., Sakiyama T., Hasegawa H., Saijo M., Maeda A., Kurane I.,
 RA Maeno G., Kimura J., Hirama C., Yoshida T., Asahi-Ozaki Y., Sata T.,
 RA Kurata T., Kojima A.;
 RT "An attenuated LC16m8 smallpox vaccine: analysis of full-genome
 sequence and induction of immune protection.";
 RL J. Virol. 79:11873-11891 (2005).
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AY678275; AAW23413.1; -; Genomic_DNA.
 DR EMBL; AY678277; AAW23695.1; -; Genomic_DNA.
 DR GO; GO:0016032; P:viral life cycle; IEA.
 DR InterPro; IPR004967; Pox_C7_F8A.
 DR Pfam; PF03287; Pox_C7_F8A; 1.
 DR PIRSF; PIRSF003779; VAC_C7L; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 150 AA; 17999 MW; 47CDF841D563C0A4 CRC64;

Query Match 100.0%; Score 9; DB 2; Length 150;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDTFYYY 9
 |||||||||
 Db 74 KVDDTFYYY 82

RESULT 8

Q6RZS8_9POXV
 ID Q6RZS8_9POXV PRELIMINARY; PRT; 150 AA.
 AC Q6RZS8;
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 9.
 DE RPXV013.
 GN ORFNames=RPXV013;
 OS Rabbitpox virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=32606;

RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=16227218; DOI=10.1099/vir.0.81331-0;
 RA Li G., Chen N., Roper R.L., Feng Z., Hunter A., Danila M.,
 RA Lefkowitz E.J., Buller R.M., Upton C.;
 RT "Complete coding sequences of the rabbitpox virus genome.";
 RL J. Gen. Virol. 86:2969-2977 (2005).
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AY484669; AAS49726.1; -; Genomic_DNA.
 DR GO; GO:0016032; P:viral life cycle; IEA.
 DR InterPro; IPR004967; Pox_C7_F8A.
 DR Pfam; PF03287; Pox_C7_F8A; 1.
 DR PIRSF; PIRSF003779; VAC_C7L; 1.
 SQ SEQUENCE 150 AA; 17999 MW; 47CDF841D563C0A4 CRC64;

Query Match 100.0%; Score 9; DB 2; Length 150;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDTFYYV 9
 |||||
 Db 74 KVDDTFYYV 82

RESULT 9
 Q76Q66_VARV
 ID Q76Q66_VARV PRELIMINARY; PRT; 150 AA.
 AC Q76Q66;
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 8.
 DE B14L protein.
 GN Name=B14L;
 OS Variola minor virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=53258;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Garcia-1966;
 RA Shchelkunov S.N., Totmenin A.V., Gutorov V.V., Safronov P.F.,
 RA Massung R.F., Loparev V.N., Knight J.C., Chizhikov V.E., Parsons J.M.,
 RA Esposito J.J., Sosnovtsev S.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; Y16780; CAB54608.1; -; Genomic_DNA.
 DR GO; GO:0016032; P:viral life cycle; IEA.
 DR InterPro; IPR004967; Pox_C7_F8A.
 DR Pfam; PF03287; Pox_C7_F8A; 1.
 DR PIRSF; PIRSF003779; VAC_C7L; 1.
 SQ SEQUENCE 150 AA; 18027 MW; 50FDF841C253CE94 CRC64;

Query Match 100.0%; Score 9; DB 2; Length 150;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDTFYYV 9
 |||||
 Db 74 KVDDTFYYV 82

Db 74 KVDDTFYYV 82

RESULT 10

Q76QL6_COWPX

ID Q76QL6_COWPX PRELIMINARY; PRT; 150 AA.
 AC Q76QL6;
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 9.
 DE C13L protein.
 GN Name=C13L;
 OS Cowpox virus (CPV).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=10243;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=GRI-90;
 RX MEDLINE=97068532; PubMed=8963248;
 RA Safronov P.F., Petrov N.A., Riazankina O.I., Totmenin A.V.,
 RA Shchelkunov S.N., Sandakhchiev L.S.;
 RT "Genes of a circle of hosts for the cowpox virus.";
 RL Dokl. Akad. Nauk SSSR 349:829-833(1996).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=GRI-90;
 RX MEDLINE=98229462; PubMed=9568042; DOI=10.1006/viro.1998.9039;
 RA Shchelkunov S.N., Safronov P.F., Totmenin A.V., Petrov N.A.,
 RA Riazankina O.I., Gutorov V.V., Kotwal G.J.;
 RT "The genomic sequence analysis of the left and right species-specific
 RT terminal region of a cowpox virus strain reveals unique sequences and
 RT a cluster of intact ORFs for immunomodulatory and host range
 RT proteins.";
 RL Virology 243:432-460(1998).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=GRI-90;
 RA Shchelkunov S.N., Safronov P.F., Totmenin A.V., Miheev M.V.,
 RA Riazankina O.I., Petrov N.A., Gutorov V.V., Kotwal G.J.,
 RA Sandakhchiev L.S.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; X94355; CAA64098.1; -; Genomic_DNA.
 DR GO; GO:0016032; P:viral life cycle; IEA.
 DR InterPro; IPR004967; Pox_C7_F8A.
 DR Pfam; PF03287; Pox_C7_F8A; 1.
 DR PIRSF; PIRSF003779; VAC_C7L; 1.
 SQ SEQUENCE 150 AA; 17999 MW; 47CDF841D563C0A4 CRC64;

Query Match 100.0%; Score 9; DB 2; Length 150;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDTFYYV 9
 | | | | | | | |
 Db 74 KVDDTFYYV 82

RESULT 11
 Q77TN9_VACCT

ID Q77TN9_VACCT PRELIMINARY; PRT; 150 AA.
 AC Q77TN9;
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 8.
 DE TC7L.
 OS Vaccinia virus (strain Tian Tan) (VACV).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=10253;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Tian Tan;
 RA Jin Q., Hou Y.D., Cheng N.H., Yao E.M., Cheng S.X., Yang X.K.,
 RA Jing D.Y., Yu W.H., Yuan J.S., Ma X.J.;
 RL Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AF095689; AAF33872.1; -; Genomic_DNA.
 DR GO; GO:0016032; P:viral life cycle; IEA.
 DR InterPro; IPR004967; Pox_C7_F8A.
 DR Pfam; PF03287; Pox_C7_F8A; 1.
 DR PIRSF; PIRSF003779; VAC_C7L; 1.
 SQ SEQUENCE 150 AA; 17999 MW; 47CDF841D563C0A4 CRC64;

Query Match 100.0%; Score 9; DB 2; Length 150;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KVDDTFYYV 9
 ||||| |||
 Db 74 KVDDTFYYV 82

RESULT 12
 Q8JLI7_9POXV
 ID Q8JLI7_9POXV PRELIMINARY; PRT; 150 AA.
 AC Q8JLI7;
 DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
 DT 01-OCT-2002, sequence version 1.
 DT 07-FEB-2006, entry version 12.
 DE EVM015.
 GN Name=EVM015;
 OS Ectromelia virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=12643;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Moscow;
 RX MEDLINE=95266283; PubMed=7747448;
 RA Mossman K., Upton C., Buller R.M., McFadden G.;
 RT "Species specificity of ectromelia virus and vaccinia virus
 RT interferon-gamma binding proteins.";
 RL Virology 208:762-769(1995).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Moscow;
 RX MEDLINE=20192152; PubMed=10725549; DOI=10.1016/S0168-1702(99)00135-5;
 RA Chen N., Buller R.M., Wall E.M., Upton C.;
 RT "Analysis of host response modifier ORFs of ectromelia virus, the
 RT causative agent of mousepox.";

RL Virus Res. 66:155-173 (2000).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Moscow;
 RX MEDLINE=98154919; PubMed=9495531; DOI=10.1016/S0168-1702(97)00122-6;
 RA Wall E.M., Cao J.X., Chen N., Buller R.M.L., Upton C.;
 RT "A novel poxvirus gene and its human homolog are similar to an E. coli
 RT lysophospholipase.";
 RL Virus Res. 52:157-167 (1997).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Moscow;
 RA Chen N., Danila M.I., Feng Z., Buller M.L., Wang C., Han X.,
 RA Lefkowitz E., Upton C.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AF012825; AAM92321.1; -; Genomic_DNA.
 DR GO; GO:0016032; P:viral life cycle; IEA.
 DR InterPro; IPR004967; Pox_C7_F8A.
 DR Pfam; PF03287; Pox_C7_F8A; 1.
 DR PIRSF; PIRSF003779; VAC_C7L; 1.
 SQ SEQUENCE 150 AA; 18130 MW; 4DD4FC55F62422BE CRC64;

Query Match 100.0%; Score 9; DB 2; Length 150;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KVDDTFYYV 9
 |||||
 Db 74 KVDDTFYYV 82

RESULT 13
 Q8QN33_COWPX
 ID Q8QN33_COWPX PRELIMINARY; PRT; 150 AA.
 AC Q8QN33;
 DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
 DT 01-JUN-2002, sequence version 1.
 DT 07-FEB-2006, entry version 10.
 DE CPXV029 protein.
 GN Name=CPXV029 CDS;
 OS Cowpox virus (CPV).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=10243;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Brighton Red;
 RX MEDLINE=83117629; PubMed=6961398;
 RA Pickup D.J., Bastia D., Stone H.O., Joklik W.K.;
 RT "Sequence of terminal regions of cowpox virus DNA: arrangement of
 RT repeated and unique sequence elements.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:7112-7116(1982).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Brighton Red;
 RX MEDLINE=90177240; PubMed=2309453;
 RA Parsons B.L., Pickup D.J.;
 RT "Transcription of orthopoxvirus telomeres at late times during
 RT infection.";
 RL Virology 175:69-80(1990).

RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Brighton Red;
 RX MEDLINE=91196263; PubMed=2014645;
 RA Hu F.Q., Pickup D.J.;
 RT "Transcription of the terminal loop region of vaccinia virus DNA is
 RT initiated from the telomere sequences directing DNA resolution.";
 RL Virology 181:716-720(1991).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Brighton Red;
 RX MEDLINE=94378510; PubMed=8091665;
 RA Hu F.Q., Smith C.A., Pickup D.J.;
 RT "Cowpox virus contains two copies of an early gene encoding a soluble
 RT secreted form of the type II TNF receptor.";
 RL Virology 204:343-356(1994).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Brighton Red;
 RA Dietrich F.S., Ray C.A., Sharma D.A., Allen A., Pickup D.J.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DDJB databases.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AF482758; AAM13476.1; -; Genomic_DNA.
 DR GO; GO:0016032; P:viral life cycle; IEA.
 DR InterPro; IPR004967; Pox_C7_F8A.
 DR Pfam; PF03287; Pox_C7_F8A; 1.
 DR PIRSF; PIRSF003779; VAC_C7L; 1.
 SQ SEQUENCE 150 AA; 17954 MW; 6B5C029714B02944 CRC64;

Query Match 100.0%; Score 9; DB 2; Length 150;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVDDTFYYV 9
 |||||
 Db 74 KVDDTFYYV 82

RESULT 14
 Q4WIR3_ASPFU
 ID Q4WIR3_ASPFU PRELIMINARY; PRT; 512 AA.
 AC Q4WIR3;
 DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2005, sequence version 1.
 DT 07-MAR-2006, entry version 6.
 DE Possible beta-xylosidase, family 43 of glycosyl hydrolases.
 GN ORFNames=Afu2g00930;
 OS Aspergillus fumigatus (Sartorya fumigata).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=5085;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Af293 / CBS 101355 / FGSC A1100;
 RX PubMed=16372009; DOI=10.1038/nature04332;
 RA Nierman W.C., Pain A., Anderson M.J., Wortman J.R., Kim H.S.,
 RA Arroyo J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.W.,
 RA Bowyer P., Chen D., Collins M., Coulsen R., Davies R., Dyer P.S.,
 RA Farman M., Fedorova N., Fedorova N.D., Feldblyum T.V., Fischer R.,
 RA Fosker N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
 RA Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.J.,

RA Haas H., Harris D.E., Horiuchi H., Huang J., Humphray S., Jimenez J.,
 RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Konzack S.,
 RA Kulkarni R., Kumagai T., Lafhton A., Latge J.-P., Li W., Lord A.,
 RA Lu C., Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M.,
 RA Monod M., Mouyna I., Mulligan S., Murphy L.D., O'Neil S., Paulsen I.,
 RA Penalva M.A., Pertea M., Price C., Pritchard B.L., Quail M.A.,
 RA Rabbinowitsch E., Rawlins N., Rajandream M.A., Reichard U.,
 RA Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
 RA Ronning C.M., Rutter S., Salzberg S.L., Sanchez M.,
 RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
 RA Takeuchi M., Tekaia F., Turner G., Vazquez de Aldana C.R., Weidman J.,
 RA White O., Woodward J.R., Yu J.-H., Fraser C.M., Galagan J.E., Asai K.,
 RA Machida M., Hall N., Barrell B.G., Denning D.W.;
 RT "Genomic sequence of the pathogenic and allergenic filamentous fungus
 Aspergillus fumigatus.";
 RL Nature 438:1151-1156 (2005).
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AAHF01000008; EAL87192.1; -; Genomic_DNA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 KW Complete proteome; Hydrolase.
 SQ SEQUENCE 512 AA; 55648 MW; 5E174A037C55B830 CRC64;

Query Match 77.8%; Score 7; DB 2; Length 512;
 Best Local Similarity 100.0%; Pred. No. 7.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTFYY 8
 |||||
 Db 26 VDDTFYY 32

RESULT 15
 Q2U7D1_ASPO
 ID Q2U7D1_ASPO PRELIMINARY; PRT; 515 AA.
 AC Q2U7D1;
 DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
 DT 24-JAN-2006, sequence version 1.
 DT 07-MAR-2006, entry version 3.
 DE Beta-xylosidase.
 GN ORFNames=AO090701000886;
 OS Aspergillus oryzae.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=5062;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=RIB 40;
 RX PubMed=16372010; DOI=10.1038/nature04300;
 RA Machida M., Asai K., Sano M., Tanaka T., Kumagai T., Terai G.,
 RA Kusumoto K., Arima T., Akita O., Kashiwagi Y., Abe K., Gomi K.,
 RA Horiuchi H., Kitamoto K., Kobayashi T., Takeuchi M., Denning D.W.,
 RA Galagan J.E., Nierman W.C., Yu J., Archer D.B., Bennett J.W.,
 RA Bhatnagar D., Cleveland T.E., Fedorova N.D., Gotoh O., Horikawa H.,
 RA Hosoyama A., Ichinomiya M., Igarashi R., Iwashita K., Juvvadi P.R.,
 RA Kato M., Kato Y., Kin T., Kokubun A., Maeda H., Maeyama N.,
 RA Maruyama J., Nagasaki H., Nakajima T., Oda K., Okada K., Paulsen I.,

RA Sakamoto K., Sawano T., Takahashi M., Takase K., Terabayashi Y.,
 RA Wortman J.R., Yamada O., Yamagata Y., Anazawa H., Hata Y., Koide Y.,
 RA Komori T., Koyama Y., Minetoki T., Suharnan S., Tanaka A., Isono K.,
 RA Kuhara S., Ogasawara N., Kikuchi H.;
 RT "Genome sequencing and analysis of *Aspergillus oryzae*.";
 RL *Nature* 438:1157-1161(2005).

CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----

DR EMBL; AP007164; BAE62534.1; -; Genomic_DNA.

SQ SEQUENCE 515 AA; 56635 MW; 3EDFD2B09FF52176 CRC64;

Query Match 77.8%; Score 7; DB 2; Length 515;
 Best Local Similarity 100.0%; Pred. No. 7.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTFYY 8
 |||||
 Db 39 VDDTFYY 45

RESULT 16

P73845_SYNY3

ID P73845_SYNY3 PRELIMINARY; PRT; 770 AA.

AC P73845;

DT 01-FEB-1997, integrated into UniProtKB/TrEMBL.

DT 01-FEB-1997, sequence version 1.

DT 07-FEB-2006, entry version 26.

DE Sll1608 protein.

GN OrderedLocusNames=sll1608;

OS *Synechocystis* sp. (strain PCC 6803).

OC Bacteria; Cyanobacteria; Chroococcales; *Synechocystis*.

OX NCBI_TaxID=1148;

RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RX MEDLINE=97061201; PubMed=8905231; DOI=10.1093/dnare/3.3.109;

RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,

RA Miyajima N., Hirose M., Sugiura M., Sasamoto S., Kimura T.,

RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,

RA Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,

RA Tabata S.;

RT "Sequence analysis of the genome of the unicellular cyanobacterium

RT *Synechocystis* sp. strain PCC6803. II. Sequence determination of the

RT entire genome and assignment of potential protein-coding regions.";

RL DNA Res. 3:109-136(1996).

CC -----

CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>

CC Distributed under the Creative Commons Attribution-NoDerivs License

CC -----

DR EMBL; BA000022; BAA17904.1; -; Genomic_DNA.

DR PIR; S75042; S75042.

DR BioCyc; SSP1148:SLL1608-MONOMER; -.

DR InterPro; IPR002931; Trnsglumase_like.

DR Pfam; PF01841; Transglut_core; 1.

DR SMART; SM00460; TGc; 1.

KW Complete proteome.

SQ SEQUENCE 770 AA; 87815 MW; F58C2EA34EC8873C CRC64;

Query Match 77.8%; Score 7; DB 2; Length 770;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDDTFYY 8

Db 286 VDDTFYY 292
 |||||

RESULT 17

Q8VUW8_STAHO

ID Q8VUW8_STAHO PRELIMINARY; PRT; 103 AA.
 AC Q8VUW8;
 DT 01-MAR-2002; integrated into UniProtKB/TrEMBL.
 DT 01-MAR-2002, sequence version 1.
 DT 07-FEB-2006, entry version 9.
 DE ORF19.
 OS Staphylococcus hominis.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1290;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=GIFU12263;
 RX MEDLINE=22586405; PubMed=12700250;
 RX DOI=10.1128/JB.185.9.2711-2722.2003;
 RA Katayama Y., Takeuchi F., Ito T., Ma X.X., Ui-Mizutani Y.,
 RA Kobayashi I., Hiramatsu K.;
 RT "Identification in methicillin-susceptible Staphylococcus hominis of
 an active primordial mobile genetic element for the staphylococcal
 RT cassette chromosome mec of methicillin-resistant Staphylococcus
 RT aureus.";
 RL J. Bacteriol. 185:2711-2722(2003).
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AB063171; BAB83490.1; -; Genomic_DNA.
 DR InterPro; IPR009303; DUF960_STA_spp.
 DR Pfam; PF06124; DUF960; 1.
 SQ SEQUENCE 103 AA; 12599 MW; 13194326CCE4617D CRC64;

Query Match 66.7%; Score 6; DB 2; Length 103;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DTFYYV 9
 |||||
 Db 91 DTFYYV 96

RESULT 18

Q38248_9CAUD

ID Q38248_9CAUD PRELIMINARY; PRT; 126 AA.
 AC Q38248;
 DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
 DT 01-NOV-1996, sequence version 1.
 DT 07-FEB-2006, entry version 16.
 DE DNA polymerase subunit.
 OS Lactococcus phage bIL67.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
 OC c2-like viruses.
 OX NCBI_TaxID=36343;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=95111629; PubMed=7812447;
 RA Schouler C., Ehrlich S.D., Chopin M.C.;
 RT "Sequence and organization of the lactococcal prolate-headed bIL67
 RT phage genome.";
 RL Microbiology 140:3061-3069 (1994).

CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; L33769; AAA74342.1; -; Genomic_DNA.
 SQ SEQUENCE 126 AA; 14843 MW; 1768C9622ED7749B CRC64;

Query Match 66.7%; Score 6; DB 2; Length 126;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KVDDTF 6 .
 |||||
 Db 100 KVDDTF 105

RESULT 19
 Q5A2T5_CANAL
 ID Q5A2T5_CANAL PRELIMINARY; PRT; 176 AA.
 AC Q5A2T5;
 DT 26-APR-2005, integrated into UniProtKB/TrEMBL.
 DT 26-APR-2005, sequence version 1.
 DT 07-FEB-2006, entry version 7.
 DE Hypothetical protein.
 GN ORFNames=CaO19.2181, CaO19.9727;
 OS Candida albicans SC5314.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 OX NCBI_TaxID=237561;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=SC5314;
 RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
 RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
 RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
 RA Davis R.W., Scherer S.;
 RT "The diploid genome sequence of Candida albicans.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334 (2004).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AACQ01000075; EAK97013.1; -; Genomic_DNA.
 DR EMBL; AACQ01000076; EAK96954.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 176 AA; 19448 MW; D04B9BE79CA86853 CRC64;

Query Match 66.7%; Score 6; DB 2; Length 176;
 Best Local Similarity 100.0%; Pred. No. 45;

[start](#) | [next page](#)



All Databases	PubMed	Nucleotide	Protein	Genome	Structure	OMIM	PMC	Journals	Books	
Search PubMed <input type="button" value="▼"/>		for <input type="text"/>						Preview	Go	Clear

Limits Preview/Index **History** Clipboard Details

[About Entrez](#)

[Text Version](#)

[Entrez PubMed](#)

[Overview](#)

[Help | FAQ](#)

[Tutorials](#)

[New/Noteworthy](#)

[E-Utilities](#)

[PubMed Services](#)

[Journals Database](#)

[MeSH Database](#)

[Single Citation Matcher](#)

[Batch Citation Matcher](#)

[Clinical Queries](#)

[Special Queries](#)

[LinkOut](#)

[My NCBI](#)

[Related Resources](#)

[Order Documents](#)

[NLM Mobile](#)

[NLM Catalog](#)

[NLM Gateway](#)

[TOXNET](#)

[Consumer Health](#)

[Clinical Alerts](#)

[ClinicalTrials.gov](#)

[PubMed Central](#)

Limits: **Entrez Date to 2004/07/26**

- Search History will be lost after eight hours of inactivity.
- Search numbers may not be continuous; all searches are represented.
- To save search indefinitely, click query # and select Save in My NCBI.
- To combine searches use #search, e.g., #2 AND #3 or click query # for more options.

Search	Most Recent Queries	Time	Result
#89	Search cytolytic and hypoxia Limits: Entrez Date to 2004/07/26	10:27:23	10
#88	Search cytolytic and hypoxia Limits: Entrez Date to 2001/09/26	10:26:06	8
#87	Search cytolysis and hypoxia Limits: Entrez Date to 2001/09/26	10:25:22	14
#86	Search oncolysis and hypoxia Limits: Entrez Date to 2001/09/26	10:25:06	0
#85	Search oncolytic and hypoxic responsive element Limits: Entrez Date to 2001/09/26	10:24:37	0
#84	Search oncolytic and hypoxia Limits: Entrez Date to 2001/09/26	10:24:11	0
#83	Search oncolytic and hypoxia responsive element Limits: Entrez Date to 2001/09/26	10:23:59	0
#69	Search Afonso C 2002 and camelpox	09:14:36	1
#68	Search Afonso C 2002	09:14:07	15
#66	Search Shchelkunov S 1998 and cowpox	08:15:10	3
#64	Search Mossman K 1995 and species	08:06:49	2
#62	Search Shchelkunov S 1993	08:01:21	14
#60	Search Massung R 1993 and potential	07:57:24	2
#53	Search Dolphin T 2000 and Tendon	07:20:18	1
#52	Search Heyes W 2000	07:19:56	1
#51	Search Heyes D 2000	07:19:38	1
#50	Search Heyes D 2000 and foot	07:19:31	0
#49	Search Heyes D 2000 and Tendon	07:19:21	0
#47	Search Sharma P 2005 and tendon	07:16:57	5
#46	Search Kumta S 2005 and management	07:16:12	1
#45	Search Maffuli N 2005 and tendinopathology	07:15:38	1
#44	Search Maffuli N 2005 and tendinopathology	07:15:22	2
#43	Search young j 2005 and ache is and tendinopathology	07:14:53	18
#42	Search Young J 2005 and achellis and tendinopathology	07:14:46	1011
#41	Search Young J 2005 and achellis	07:14:29	1011

<u>#40</u> Search Young J 2005 and achelles	07:14:20	<u>1011</u>
<u>#39</u> Search Young J 2005 and Healing	07:13:48	<u>10</u>
<u>#37</u> Search Beredjiklian P 2003 and tendon	07:11:28	<u>3</u>
<u>#35</u> Search Buckwalter J 1999 and implications	07:10:01	<u>2</u>
<u>#33</u> Search Woo S 1999 and Tissue	07:08:35	<u>20</u>
<u>#32</u> Search Woo L 1999 and Tissue	07:08:30	<u>0</u>
<u>#31</u> Search Woo L 1999 and Tissue engineering	07:08:23	<u>0</u>
<u>#30</u> Search Butler D 1999 and Perspectives	07:07:00	<u>1</u>
<u>#29</u> Search Buterr D 1999 and Perspectives	07:06:46	<u>58</u>
<u>#27</u> Search Carpenter J 1999 and animal model	07:05:25	<u>4</u>
<u>#26</u> Search Carpenter J 1999	07:05:11	<u>71</u>
<u>#24</u> Search jarvinen t 2000 and tenascin	07:02:38	<u>2</u>
<u>#23</u> Search Jarvine T 2000 and Tanascin	07:02:35	<u>0</u>
<u>#21</u> Search woo S 2000 and Injury	07:00:55	<u>15</u>
<u>#19</u> Search speed c 2001 and therapeutic	06:56:22	<u>3</u>
<u>#18</u> Search Spped C 2001 and Therapeutic	06:56:20	<u>0</u>
<u>#14</u> Search McCue T 2002 and Achilles	06:51:06	<u>1</u>
<u>#13</u> Search McCue T 2003 and Achilles	06:50:49	<u>0</u>
<u>#12</u> Search Fenwick S 2002 and vasculature	06:49:00	<u>1</u>
<u>#11</u> Search Purdam C 2003 and Achilles	06:47:40	<u>1</u>
<u>#10</u> Search Paavola M 2002 and corticosteroid	06:43:38	<u>1</u>
<u>#9</u> Search Almekinders L 2003 and compression	06:40:16	<u>1</u>
<u>#7</u> Search Lin T 2004 and Tendon	06:34:06	<u>7</u>
<u>#6</u> Search Lin T 2004 and Biomechanics	06:33:43	<u>70</u>
<u>#5</u> Search Brown J and ankle	06:32:28	<u>20</u>
<u>#4</u> Search Brown J 2004 and ankle	06:32:18	<u>18</u>
<u>#3</u> Search Brown D 2004 and ankle	06:32:08	<u>5</u>
<u>#2</u> Search Micheli J 2004 and ankle	06:31:53	<u>0</u>
<u>#1</u> Search Brown T 2004 and ankle	06:30:54	<u>14</u>

[Clear History](#)

[Write to the Help Desk](#)

[NCBI](#) | [NLM](#) | [NIH](#)

[Department of Health & Human Services](#)

[Privacy Statement](#) | [Freedom of Information Act](#) | [Disclaimer](#)

Nov 27 2006 08:22:25